**Codes used to pre-process and assemble the genomes of *M. morganii***

**Filtration**

Command line: java -jar trimmomatic-0.36. jar SE -phred33 reads\_R2.fastq.gz reads\_R2\_filtrated.fq CROP:244 HEADCROP:5

**Genome assembly**

Command line: spades.py -1 reads\_R1.fq -2 reads\_R2.fq --careful -o output\_dir -t8 -m256

System information:

SPAdes version: 3.10.0

Python version: 2.7.12

OS: Linux-4.4.0-103-generic-x86\_64-with-Ubuntu-16.04-xenial

Mode: read error correction and assembling

Debug mode is turned OFF